

Shared Resources

Shared Resources Provide Leading-Edge Research Tools

Researchers at UCLA's Jonsson Comprehensive Cancer Center have access to a remarkable array of tools that can aid in speeding discovery of newer and more effective ways to treat cancer.

Through the 10 shared resources provided by the cancer center, scientists can screen 100,000 compounds in a day, conduct clinical trials of promising, novel experimental therapies and conduct whole genome analyses using DNA microarrays.

"The cancer center leadership strongly believes it is important to provide access to technology that might not otherwise be available to our scientists," said Harvey Herschman, director of basic research programs at the cancer center. "The idea of these shared resources is to supply a sort of one-stop-shopping for cancer center members, making it easier for them to do their science and making them more productive. That way, everyone doesn't have to reinvent the wheel."



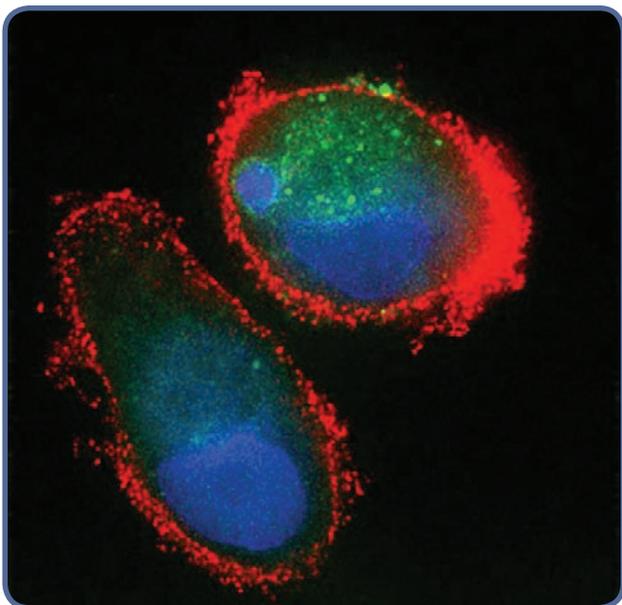
Shared Resources include:

Biostatistics, Analytical Support & Evaluation (BASE) Unit

Director – Gang Li

Co-director – Robert Elashoff

This shared resource was established in 1994 to provide the highest quality biostatistical support to cancer-related research, including basic science, clinical and translational research and cancer prevention and control research at UCLA. BASE offers a group of highly regarded statistics faculty and staff with expertise in variety of areas, including biostatistical methods for the design and analysis of clinical trials, survival analysis, longitudinal data analysis, imaging analysis, missing data and high-throughput data such as microarray data. Biostatisticians of BASE participate and help in all phases of cancer research, from study design in the planning stage, monitoring and implementing the study, to the analysis, interpretation and reporting of study results. BASE also develops novel statistical methodology when needed in cancer center studies. BASE Unit members develop various educational programs including courses, seminars and short presentations for investigators. BASE also provides and maintains the necessary computer equipment and software for computerized data analysis and management, for general biostatistical methodology and specialty areas such as pharmacokinetics, tissue array, microarray gene expression, clinical trials, imaging, repeated measures and survey methods.



Clinical Research Unit

Director – Dr. Sara Hurvitz

The Clinical Research Unit (CRU) Shared Resource provides administrative oversight of cancer center studies conducted both on campus and in the Translational Oncology Research International (TORI) network. Services to investigators include providing trained research nurses, coordinators, data managers and regulatory coordinators to conduct the clinical trials, with priority given to translational/institutional studies, followed by cooperative group, then industry-sponsored but under-funded innovative research. In addition, consultation services are available for new and/or junior investigators to develop clinical research protocols, review sponsored research and provide guidance in budgets and study logistics. Monitoring and auditing of investigator-initiated and sponsored studies is provided to ensure uniform scientific merit, patient safety, quality assurance and compliance. UCLA investigators collaborate with research institutions and health care providers across the United States in order to offer translational oncology research studies to patients in their own communities through the TORI network. Under the supervision of the CRU leadership, patients at TORI community locations can participate in the same high quality, leading-edge research studies that are available in our campus-based clinical trials program.

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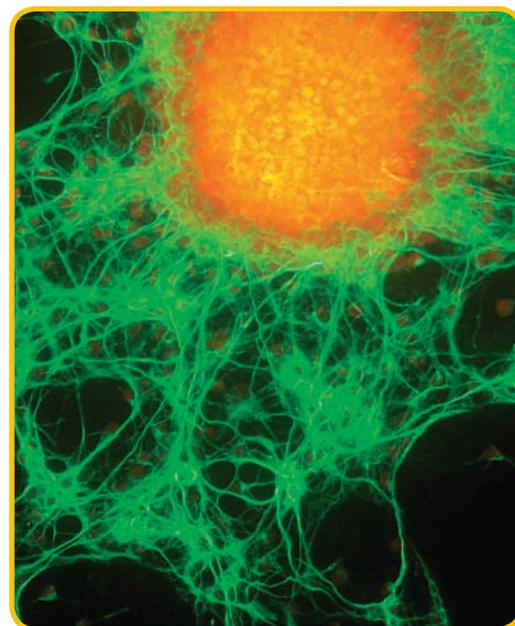
ES Cell/Transgenic Mice

Director – Dr. Hong Wu

Co-Director - Dr. Xin Liu

Co-Director - Meisheng Jiang

The mouse is the most useful animal model for most cancers, because it recapitulates the major features of human malignancies. Recent technological breakthroughs allow for mouse genome manipulation, such as removing, adding or changing a specific gene or installing a gene “on and off” switch in the genome, providing powerful tools for studying the causes and development of cancers in a living organism. This shared resource provides access to the latest technology for generating a variety of genetically modified animal models for research. One service provided is a transgenic service that generates animal models by introducing genetic information directly into the genome. The other service allows germ line manipulation via embryonic stem cells. The use of transgenic animals and of germ line manipulation for the creation of mutations has resulted in many mouse models for cancer research. The generation of mouse models that lack genes that encode proteins of oncological interest or tumor suppressor ability has proven to be a useful way of elucidating gene function *in vivo*. Transgenic mouse models, which have extra copies of either functional or dysfunctional genes, have provided important insight into the complex events contributing to cellular de-regulation and the loss of growth control that can lead to cancer. Animal model studies contribute greatly to the identification and characterization of proteins that contribute to the development of cancer.

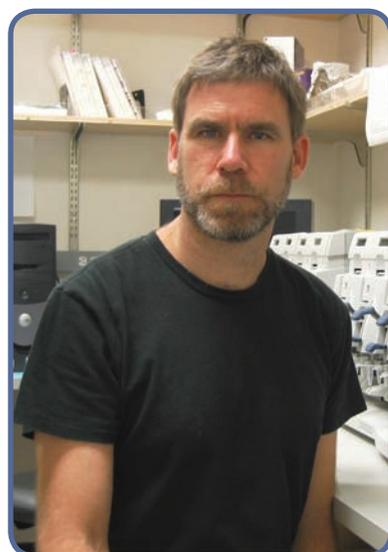


Flow Cytometry

Director – Beth Jamieson

Manager – Ingrid Schmid

The flow cytometry shared resource allows researchers to count and examine cells and other particles suspended in fluid. Laser light is aimed at cells suspended in a focused liquid stream. Each cell scatters the laser light and fluorescent probes that are either directly bound to cellular components or are conjugated to reagents bound to cell structures excited by the laser light to emit fluorescence at a longer wavelength specific for the fluorochrome. The combination of scattered and fluorescent light signals is recorded by detectors and converted into images on computer screens. A special flow cytometer called a cell sorter not only analyzes cells, but also can physically separate cells which differ in scatter and fluorescent properties, allowing further study of the isolated sub-populations. Flow cytometry permits rapid analysis and separation of complex cell mixtures into cell populations with differing properties. The shared resource houses five analytical flow cytometers and three high-speed cell sorters with different color lasers to assist UCLA cancer researchers with their experimental needs. Equally as important as the state-of-the-art instrumentation are the consultation and training available. Staff members provide help with designing experiments and develop or adapt new flow cytometry methods. Classes in basic flow cytometry principles and hands-on training in running samples on the analyzers offer an opportunity for researchers to discover the potential of flow cytometry and acquire skills that serve them throughout their careers.



Gene Expression

Director – Dr. Stanley Nelson

Co-director – Dr. Christopher Denny

The Gene Expression Shared Resource offers whole genome analyses using DNA microarrays. Services include the ability to assess whether individual genes are on or off in cancers and other cell types. This data gives biologists critical information about which genes within the genome are active in a given process such as cancer. Microarrays are a powerful technology that allow millions of different probes to be designed throughout the entire genome so that every gene can be simultaneously assessed at a modest cost. The shared resource offers the ability to process these complex experiments with materials provided by scientists, expanding their arsenal of tools available to study cancer. The resource also offers microarray services that permit the entire genome to be assessed for DNA mutations critical in cancer formation, created by the mutation of an unknown number of genes that change a normal cell into a cancerous clone that grows, divides and spreads uncontrollably. Understanding the exact mutations that occur within the cancers provides key insights into how they develop and thus provides insight as to how to create novel therapies. The resource has recently implemented massively parallel sequencing that can simultaneously sequence every gene in individual cancers. The first cancer cell line completely sequenced was completed using the resource. These studies are revealing the fundamental basis of various cancers.

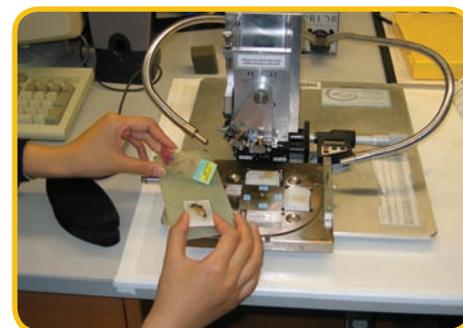
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Informatics

Director – Dr. Arash Naeim

Associate director – Courtney Martin

Informatics is focused on supporting the cancer center in its effort to collect, process, share and use data electronically. Currently, a clinical trials management system, Velos eResearch, is being implemented. This electronic system allows for the central management of clinical trials study and patient information, providing real time tracking, auditing and resource management. The study and patient information managed are critical for required National Cancer Institute (NCI) annual reports. As the system expands, additional functionality will be incorporated to allow the cancer center to share clinical data collaboratively with the NCI and other cancer centers. This effort is part of a larger initiative to determine the best ways to electronically capture patient, treatment and specimen data. Other ongoing projects with some Informatics office involvement include deploying a new electronic medical record system, Varian, and implementing a tissue bank, Daedalus. In addition to developing collaborative relationships with industry-leading software companies, the Informatics group is working with the cancer center community and NCI to test new open source tools and share data in a national grid. Additionally, the Informatics group is supporting the development of electronic repositories of data for the Avon Cares for Life project, the UCLA Sarcoma Group and has just started on a University of California effort called ATHENA to advance treatment and research in breast cancer.

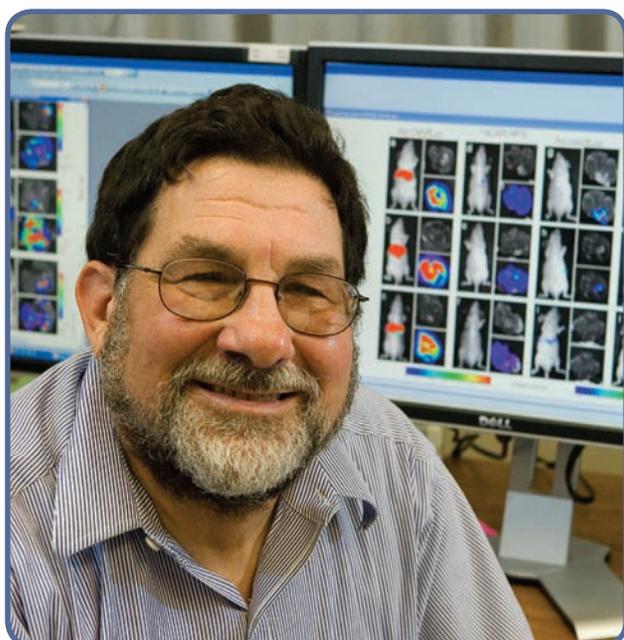


Molecular Screening

Director – Kenneth Bradley

Co-director – Robert Damoiseaux

The state-of-the-art molecular screening shared resource can screen as many as 100,000 compounds in a day, a manual process that used to take years. The compounds - small molecule drugs already approved by the FDA as well as purified natural products and fully synthetic molecules - come to UCLA from all over the world or are developed by UCLA chemists. Researchers can use the resource to test cancer cell lines developed in their laboratories. The researcher with the assistance of shared resource staff develops an assay, a procedure in molecular biology to test or measure the activity of a drug or biochemical compound in an organic sample, in this case the cancer cell lines. The cells are loaded into plates with 384 wells each and the drugs are added. After the assay is performed and success with a small library of compounds is achieved, up to 90,000 compounds can be screened against the cell lines in an effort to find one that may be developed into a cancer therapy. A computerized, robotic system executes the screening process, adding the compounds to the cancer cells. A robotic arm with an automated liquid transfer system places a miniscule amount of the compound onto plate containing the cancer cells. The cells are checked after 48 hours to see if any of the compounds showed activity. For more information on the shared resource, see this [LINK](#).



Small Animal Imaging

Director – Harvey Herschman

Co-director – David Stout

A highly used shared resource on campus for cancer researchers is the small animal imaging center, which supports *in vivo* molecular imaging, primarily of metabolic function, using PET, CT, bioluminescent and fluorescent optical methods and autoradiography. Investigators have access to the equipment and protocols, as well as the expertise of the imaging center staff, who have worked together for more than 19 years. The ability to measure metabolism in mice and rats has been made possible through development of small animal imaging systems such as the microPET system, created at UCLA in the mid-1990's. Optical imaging was also introduced very early after its development and has become a proven low cost, high-throughput way to observe tumor growth and treatment effect in living animals. The center also has pioneered ways to create a safe, pathogen free environment using gas anesthesia and temperature control to ensure animals are kept at near normal physiological conditions. The creation of reproducible ways to conduct imaging with minimal impact on the animals means that fewer experiments are needed and better data can be obtained through use of the same subject multiple times in the same experiment. Findings from research in the imaging center often are directly put into use in clinical settings to better measure and understand the mechanism of disease and treatment.

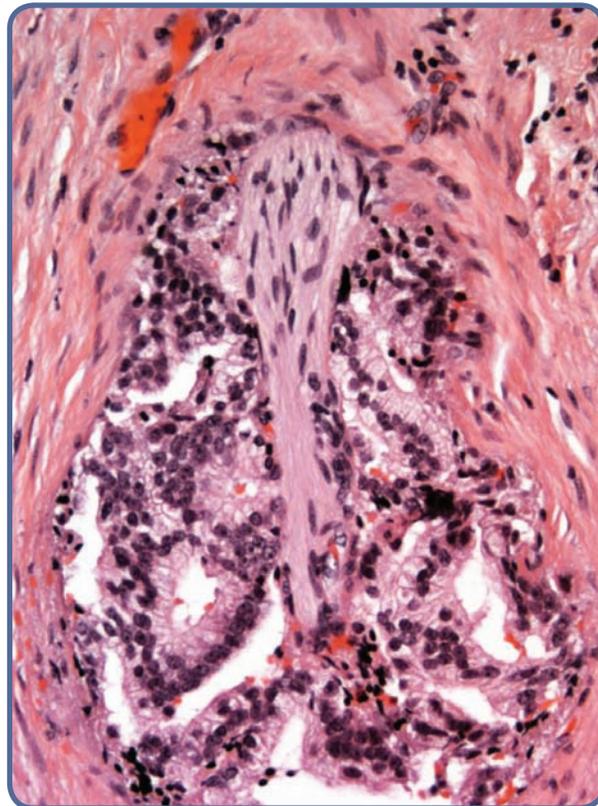
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Translational Pathology

Director – Dr. Sarah Dry

Co-director – Dr. Jonathan Said

The translational pathology shared resource facilitates research using human cancer tissues with the aim of performing translational research. Most of this tissue, collected with a patient's consent, is derived from left over tissues after surgery and would otherwise be discarded. Researchers can then perform a wide variety of experimental modalities, including genetic testing, an essential part of cancer research. The tissues also are essential for research on specific tumor markers, which can be used to diagnose cancer, follow tumor progression and predict response to specific therapies. In addition to collecting tissues, the shared resource offers services related to the handling and processing of tissues. The pathologists and technologists providing services are specially trained and experienced with all aspects of tissue processing. It also offers state-of-the-art technology, including new methods to convert microscope slides into computerized images for sophisticated image analysis. Additionally, laser-capture micro-dissection enables researchers to extract small numbers of cancer cells from the specimen, which can be submitted for analysis. In addition, shared resource staffers are available for consultation regarding tissue procurement and processing. The shared resource also provides immunohistochemistry, a tool for studying cancer tissues to determine expression of markers that aid in understanding cancer biology, assist with cancer diagnosis and predict tumor outcome or response to treatment.



Vector Core

Director – Dr. Nori Kasahara

Co-director – Christopher Logg

The mission of this shared resource is to facilitate basic and translational research by providing investigators with access to viral vectors, which are used to deliver genes into cells. The resource provides, at minimal cost, various retrovirus, lentivirus and adenovirus-based vector stocks expressing standard reporter genes for use in “gene-marking” experiments to trace the fate of specific cells, as well as a library of available pre-made vectors that already express various mammalian genes and corresponding inhibitory sequences. It also constructs and produces custom viral vectors that contain a specific sequence of interest for individual researchers and provides an educational and advisory resource to assist with safe use and handling of viral vectors, and with regulatory compliance and grant proposal submissions. Easy access to these technologies can facilitate and expand the scope of research activities, and provide ways for investigators to rapidly generate preliminary data. The shared resource also helps increase research productivity and assists in their efforts to understand the functional significance of specific genes during normal growth and development, to determine the contribution of specific genes to the pathogenesis or amelioration of malignant diseases, and to identify and validate novel therapeutic targets for conventional and genetic therapies.